> **This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

Corrected Diskette Needed *Does Not Comply*

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5       (i) APPLICANT: DOUGLAS SMITH
 6
 7      (ii) TITLE OF INVENTION:NUCLEIC ACID AND AMINO ACID SEQUENCES
 8           RELATING TO HELICOBACTER PYLORI FOR
 9           DIAGNOSTICS AND THERAPEUTICS
10
11     (iii) NUMBER OF SEQUENCES:  880
12
13      (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: LAHIVE & COCKFIELD
15           (B) STREET: 60 State Street
16           (C) CITY: Boston
17           (D) STATE: Massachusetts
18           (E) COUNTRY: USA
19           (F) ZIP: 02109-1875
20
21       (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Floppy disk
23           (B) COMPUTER: IBM PC compatible
24           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27      (vi) CURRENT APPLICATION DATA:
28           (A) APPLICATION NUMBER: US 08/487,032
29           (B) FILING DATE: 07-JUNE-1995
30
31    (viii) ATTORNEY/AGENT INFORMATION:
32           (A) NAME: Mandragouras, Amy E.
33           (B) REGISTRATION NUMBER: 36,207
34           (C) REFERENCE/DOCKET NUMBER: GTN-001
35
36      (ix) TELECOMMUNICATION INFORMATION:
37           (A) TELEPHONE: (617)227-7400
38           (B) TELEFAX: (617)227-5941
39
40
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40867    (2) INFORMATION FOR SEQ ID NO:880:
40868
40869        (i) SEQUENCE CHARACTERISTICS:
40870            (A) LENGTH: 363 amino acids
40871            (B) TYPE: amino acid
40872            (D) TOPOLOGY: linear
40873
40874       (ii) MOLECULE TYPE: protein
40875
40876      (iii) HYPOTHETICAL: YES
40877
40878       (vi) ORIGINAL SOURCE:
40879            (A) ORGANISM: Helicobacter pylori
40880
40881       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:
40882
40883    Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Xaa Phe Leu Asn Thr Gln
40884    1               5                   10                  15
40885
40886    Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
40887                20                  25                  30
40888
40889    Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
40890            35                  40                  45
40891
40892    Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
40893        50                  55                  60
40894
40895    Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
40896    65                  70                  75                  80
40897
40898    Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
40899                85                  90                  95
40900
40901    Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
40902                100                 105                 110
40903
40904    Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
40905            115                 120                 125
40906
40907    Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
40908            130                 135                 140
40909
40910    Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
40911    145                 150                 155                 160
40912
40913    Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
40914                165                 170                 175
40915
40916    Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
40917                180                 185                 190
40918
40919    Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
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40920              195                200                205
40921
40922    Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
40923        210                215                220
40924
40925    Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
40926    225                230                235                240
40927
40928    Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
40929            245                250                255
40930
40931    Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
40932            260                265                270
40933
40934    Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu
40935        275                280                285
40936
40937    Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
40938        290                295                300
40939
40940    Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser
40941    305                310                315                320
40942
40943    Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
40944                325                330                335
40945
40946    Xaa Lys Xaa Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
40947            340                345                350
40948
40949    Lys Thr Gln Xaa Arg Met Ile Xaa Gly Cys Xaa
40950            355                360
40951    {PAGE|782}
40952
40953
40954
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--> 40951 {PAGE|782} *delete*

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/487,032A*

Line	Error	Original Text
40951	Wrong Amino Acid Designator	{PAGE|782}